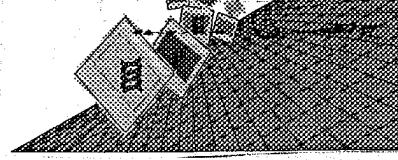


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0280

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/692,077

Source: O/PE

Date Processed by STIC: 11/2/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

invalid format for entire sequence listing 09/6/92, 077 1

Does Not Comply
Corrected Diskette Needed

L1107 L insert numeric identifier and apparent name
Application Project delete

<120> Title: Alpha-2B-Adrenergic Receptor Polymorphisms

<130> AppFileReference: 13105

<140> CurrentAppNumber:

<141> CurrentFilingDate:

L1607 L insert numeric identifier and total number of sequenced figure
Sequence L2107 1
L2117 1353
L2127 DNA

<213> OrganismName: Homo sapiens

<400> PreSequenceString: 1

ATGGACCACG AGGACCCCTA CTCCGTGCAG GCCACAGCGG CCATAGCGGC GGCCATCACC ← 60 insert
← 60 TTCCTCATTC TCTTACCAT CTTCGGCAAC GCTCTGGTCA TCCTGGCTGT GTTGACCCAGC ← 120 cumulative
120 CGCTCGCTGC CGCCCCCTCA GAACCTGTTCTCGC TGGCCGCCGC CGACATCCTG
180 GTGGCCACGC TCATCATCCC TTTCTCGCTG GCCAACGAGC TGCTGGCTA CTGGTACTTC
240 CGGCGCACGT GGTGCGAGGT GTACCTGGCG CTCGACGTGC TCTTCTGCAC CTCGTCCATC
300 GTGCACCTGT GCGCCATCAG CCTGGACCGC TACTGGCCCG TGAGCCGC GCTGGAGTAC
360 AACTCCAAGC GCACCCCGCG CCGCATCAAG TGCACTCATCC TCACTGTGTG GCTCATCGCC
420 GCCGTACATCT CGCTGCCGCC CCTCATCTAC AAGGGCGACC AGGGCCCCCA GCCGCGCGGG
480 CGCCCCCAGT GCAAGCTCAA CCAGGAGGCC TGGTACATCC TGGCCTCCAG CATCGGATCT
540 TTCTTGCTC CTTGCCTCAT CATGATCCTT GTCTACCTGC GCATCTACCT GATCGCCAAA
600 CGCAGCAACC GCAGAGGTCC CAGGGCCAAG GGGGGCCCTG GGCAGGGTGA GTCCAAGCAG
660 CCCCGACCCG ACCATGGTGG GGCTTGGCC TCAGCCAAAC TGCCAGCCCT GGCCTCTGTG
720 GCTTCTGCCA GAGAGGTCAA CGGACACTCG AAGTCCACTG GGGAGAAGGA GGAGGGGGAG
780 ACCCCTGAAG ATACTGGGAC CCGGGCCCTTG CCACCCAGTT GGGCTGCCCT TCCCAACTCA
840 GGCCAGGGCC AGAAGGGAGG TGTTTGTGGG GCATCTCCAG AGGATGAAGC TGAAGAGGGAG
900 GAAGAGGAGG AGGAGGAGGA GGAAGAGTGT GAACCCCAAG CAGTGCAGT GTCTCCGGCC
960 CAGCTTGCA GCCCCCGCT GCAGCAGCCA CAGGGCTCCC GGGTGTGGC CACCCCTACGT
1020 GGCCAGGTGC TCCTGGGAG GGGCGTGGGT GCTATAGGTG GGCAGTGGTG GCGTCGAAGG
1080 GCGCAGCTGA CCCGGGAGAA GCGCTTCACC TTCGTGCTGG CTGTGGTCAT TGGCGTTTTT
1140 GTGCTCTGCT GGTCCCCCTT CTTCTTCAGC TACAGCCTGG GCGCCATCTG CCCGAAGCAC
1200 GTCAAGGTGC CCCATGGCCT CTTCCAGTTC TTCTTCTGGA TCGGCTACTG CAACAGCTCA
1260 CTGAACCCCTG TTATCTACAC CATCTCAAC CAGGACTTCC GCCGTGCCCT CGGGAGGATC
1320 CTGTGCCGCC CGTGGACCCA GACGGCCTGG TGA

<212> Type: DNA

<211> Length: 1353

SequenceName: Sequence 1

SequenceDescription:

L2107 2

Custom Codon

Sequence Name: Sequence 1

L2117 1344

L2127 DNA

Sequence:

<213> OrganismName: Homo sapiens

<400> PreSequenceString: 2

ATGGACCACG AGGACCCCTA CTCCGTGCAG GCCACAGCGG CCATAGCGGC GGCCATCACC
60 TTCCTCATTC TCTTACCAT CTTCGGCAAC GCTCTGGTCA TCCTGGCTGT GTTGACCCAGC
120 CGCTCGCTGC CGCCCCCTCA GAACCTGTTCTCGC TGGCCGCCGC CGACATCCTG
180 GTGGCCACGC TCATCATCCC TTTCTCGCTG GCCAACGAGC TGCTGGCTA CTGGTACTTC
240 CGGCGCACGT GGTGCGAGGT GTACCTGGCG CTCGACGTGC TCTTCTGCAC CTCGTCCATC
300 GTGCACCTGT GCGCCATCAG CCTGGACCGC TACTGGCCCG TGAGCCGC GCTGGAGTAC
360 AACTCCAAGC GCACCCCGCG CCGCATCAAG TGCACTCATCC TCACTGTGTG GCTCATCGCC
420 GCCGTACATCT CGCTGCCGCC CCTCATCTAC AAGGGCGACC AGGGCCCCCA GCCGCGCGGG
480 CGCCCCCAGT GCAAGCTCAA CCAGGAGGCC TGGTACATCC TGGCCTCCAG CATCGGATCT
540 TTCTTGCTC CTTGCCTCAT CATGATCCTT GTCTACCTGC GCATCTACCT GATCGCCAAA

delete totals ← 60 insert
base totals ← 120 cumulative
at right margin of
lock line -

DO NOT use
upper-case base
letters in
new sequence
Rules format.
use lower-case

1353

letters
for bases

insert
cumulative
base totals
at right
margin and
use lower-case
letters
for bases

09/692,077

2

delete

600 CGCAGCAACC GCAGAGGTCC CAGGGCCAAG GGGGGGCCTG GGCAGGGTGA GTCCAAGCAG
660 CCCCGACCCG ACCATGGTGG GGCTTTGGCC TCAGCCAAAC TGCCAGCCCT GGCTCTGTG
720 GCTTCTGCCA GAGAGGTCAA CGGACACTCG AAGTCCACTG GGGAGAAGGA GGAGGGGGAG
780 ACCCCTGAAG ATACTGGGAC CCGGGCCTTG CCACCCAGTT GGGCTGCCCT TCCCAACTCA
840 GCCCAGGGCC AGAAGGAGGG TGTTTGTGGG GCATCTCCAG AGGATGAAGC TGAAGAGGGAG
900 GAGGAGGAGG AGGAAGAGTG TGAACCCCAG GCAGTGCCAG TGTCTCCGGC CTCAGCTTGC
960 AGCCCCCCCAG TGCAGCAGCC ACAGGGCTCC CGGGTGCTGG CCACCCCTACG TGGCCAGGTG
1020 CCTCTGGGCA GGGCGTGGG TGCTATAGGT GGGCAGTGGT GGCGTCGAAG GGCGCAGCTG
1080 ACCCGGGAGA AGCGCTTCAC CTTCGTGCTG GCTGTGGTCA TTGGCGTTT TGTGCTCTGC
1140 TGGTTCCCCT TCTTCTTCAG CTACAGCCTG GGCGCCATCT GCCCAGAGCA CTGCAAGGTG
1200 CCCCATGGCC TCTTCCAGTT CTTCTCTGG ATCGGCTACT GCAACAGCTC ACTGAACCT
1260 GTTATCTACA CCATCTCAA CCAGGACTTC CGCCGTGCCT TCCGGAGGAT CCTGTGCCGC
1320 CCGTGGACCC AGACGGCCTG GTGA

<212> Type : DNA

<211> Length : 1344

SequenceName : Sequence 2

SequenceDescription :

Custom Codon

Sequence Name : Sequence 2

1344

*insert base
to tail and
use
lowercase
letters.*

see next page

09/692,077 3

L2107 7
L2117 450
L2127 PRT
Sequence

<213> OrganismName : Homo sapiens

<400> PreSequenceString : 7

MDHQDPYSVQ ATAAIAAAIT FILIFTIFGN ALVILAVLTS RSLRAPQNLF LVSLAAADIL
60 VATLIIPFSL ANELLGYWYF RRTWCEVYLA LDVLFCSSI VHLCAISLDR YWAVSRALEY
120 NSKRTPRRIK CIIITVWLIA AVISLPLIY KGDQGPQPRG RPQCKLNQEA WYLASSIGS
180 FFAPCLIMIL VYLRIYLIAK RSNRRGPRAK GGGQGESKQ PRPDHGGALA SAKLPALASV
240 ASAREVNHS KSTGEKEEGE TPEDTGTRAL PPSWAALPNS GQGQKEGVCG ASPEDEAEVE
300 EEEEEEEEC EPQAVPVSPA SACSPPLQQP QGSRVLATLR GQVLLGRGVG AIGGQWWRRR
360 AQLTREKRFT FVLAVVIGVF VLCWFPEFFS YSLGAICPKH CKVPHGLFQF FFWIGYCNSS
420 LNPVIYTIFN QDFRRAFRRI LCRPWTQTAW

<212> Type : PRT

<211> Length : 450

SequenceName : Sequence 7

SequenceDescription :

per sequence rules, use
three-letter amino
acid code and number
separated by space
every 5 amino
acids.

450 Delete

Do NOT use
TAB codes
between amino
acid nos. Use
space characters.

a maximum of
16 amino acids
per line allowed.

FYI: only three sequences shown as a sample
of global errors in the entire sequence
Listing. Please consult new Sequence
Rules for acceptable format, and consult
sample sequence Listing, attached.

FYI

Please review the

Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Appendix A To Subpart C to Part I—Sample Sequence Listing

<110> Smith, John

Smith, Jane

<120> Example of a Sequence Listing

<130> 01-00001

<140> US 08/999,999

<141> 1998-02-28

<150> EP 91000000

<151> 1997-12-31

Consult

<160> 2

<170> PatentIn ver. 2.0

<210> 1

<211> 403

<212> DNA

<213> *Paramecium aurelia*

<220>

<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a
Protease from *Paramecium* sp.

<303> Journal of Fictional Genes

<304> 1

<305> 1

<306> I - 7

<307> 1988-06-20

<400> 1

ctactctact ctactttcat ctactatctt ctttggatct ctgagtcgtc ctgagtggta 60

ctcttgagtc ctggagatct ctccctcac atgtgatcgat cgagactgac cgatagatcg 120

ctgactgact ctgagatagt cgagcccgta cgagaccgt cgagggtgac agagagtggg 180

cgcgtgcgcg cagagcgccg cgccggcg cgcgcgactg cgccgtggc cgcgcgagg 240

ctttcgccgc agcggcggcg ctttccggcg cgcgcggc cgcgcgatgt 300

cttctcttcc ctcccttca ctagagaggt ctatataac atg gtt tca atg ttc 355

Met Val Ser Met Phe

1

5

agc ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtc tgtttgc tc 403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

- 10

15

<210> 2

<211> 18

<212> PRT

<213> Paramecium aurelia

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1

5

10

15

Phe Val

ed: May 22, 1998.

A. Lehman,

Assistant Secretary of Commerce and
Commissioner of Patents and Trademarks.

oc. 98-14194 Filed 5-29-98; 8:45 am]

1 CODE 3510-16-C

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	'Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names, and/or Initials.'	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd.	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOS	Count includes total number of SEQ ID NOS	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	
<223>	Other Information	Other relevant information; four lines maximum	base was used in a sequence
			M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	O
<302>	Title		O
<303>	Journal		O
<304>	Volume		O
<305>	Issue		O
<306>	Pages		O
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	O
<308>	Database Accession Number	Accession number assigned by database including database name	O
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	O
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	O

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd
<313>	Relevant Residues	FROM (position) TO (position)
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;